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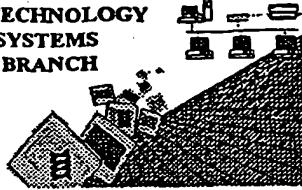
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Input Set : A:\1625seq.001
Output Set: N:\CRF4\08112003\J612466.raw

62 Asn	Gly	Tyr	Met	Arg	Ile	Thr	Asn	Glu	Asn	Phe	Val	Asp	Ala	Tyr	Glu		
63			95				100				105						
65	aac	tcc	aac	tcc	act	gag	ttt	gta	agc	ctg	gcc	agc	aag	gtg	aag	gac	388
66	Asn	Ser	Asn	Ser	Thr	Glu	Phe	Val	Ser	Leu	Ala	Ser	Lys	Val	Lys	Asp	
67			110				115				120						
69	gcg	ctg	aag	ctg	ctg	tac	agc	gga	gtc	cca	ttc	ctg	ggc	ccc	tac	cac	436
70	Ala	Leu	Lys	Leu	Leu	Tyr	Ser	Gly	Val	Pro	Phe	Leu	Gly	Pro	Tyr	His	
71			125				130			135							
73	aag	gag	tcg	gct	gtg	acg	gcc	ttc	agc	gag	ggc	agc	gtc	atc	gcc	tac	484
74	Lys	Glu	Ser	Ala	Val	Thr	Ala	Phe	Ser	Glu	Gly	Ser	Val	Ile	Ala	Tyr	
75			140			145				150							
77	tac	tgg	tct	gag	ttc	agc	atc	ccg	cag	cac	ctg	gtg	gag	gag	gcc	gag	532
78	Tyr	Trp	Ser	Glu	Phe	Ser	Val	Ile	Pro	Gln	His	Leu	Val	Glu	Glu	Ala	
79	155			160			165			170							
81	cgc	gtc	atg	gcc	gag	gag	cgc	gtc	atg	ctg	ccc	ccg	ccg	gcc	ccg	cgc	580
82	Arg	Val	Met	Ala	Glu	Glu	Arg	Val	Val	Met	Leu	Pro	Pro	Arg	Ala	Arg	
83			175			180			185								
85	tcc	ctg	aag	tcc	ttt	gtg	gtc	acc	tca	gtg	gtg	gct	ttc	ccc	acg	gac	628
86	Ser	Leu	Lys	Ser	Phe	Val	Val	Thr	Ser	Val	Val	Ala	Phe	Pro	Thr	Asp	
87			190			195			200								
89	tcc	aaa	aca	gta	cag	agg	acc	cag	gac	aac	agc	tgc	agc	ttt	ggc	ctg	676
90	Ser	Lys	Thr	Val	Gln	Arg	Thr	Gln	Asp	Asn	Ser	Cys	Ser	Phe	Gly	Leu	
91	205			210			215										
93	cac	gcc	cgc	ggc	gtg	gag	ctg	atg	cgc	ttc	acc	acg	ccc	ggc	ttc	cct	724
94	His	Ala	Arg	Gly	Val	Glu	Leu	Met	Arg	Phe	Thr	Thr	Pro	Gly	Phe	Pro	
95	220			225			230										
97	gac	agc	ccc	tac	ccc	gct	cat	gcc	cgc	tgc	cag	tgg	gcc	ctg	ccg	ggg	772
98	Asp	Ser	Pro	Tyr	Pro	Ala	His	Ala	Arg	Cys	Gln	Trp	Ala	Leu	Arg	Gly	
99	235			240			245			250							
101	gac	gcc	gac	tca	gtg	ctg	agc	ctc	acc	ttc	cgc	agc	ttt	gac	ctt	gcg	820
102	Asp	Ala	Asp	Ser	Val	Leu	Ser	Leu	Thr	Phe	Arg	Ser	Phe	Asp	Leu	Ala	
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106	Ser	Cys	Asp	Glu	Arg	Gly	Ser	Asp	Leu	Val	Thr	Val	Tyr	Asn	Thr	Leu	
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109	agc	ccc	atg	gag	ccc	cac	gcc	ctg	gtg	cag	ttg	tgt	ggc	acc	tac	cct	916
110	Ser	Pro	Met	Glu	Pro	His	Ala	Leu	Val	Gln	Leu	Cys	Gly	Thr	Tyr	Pro	
111	285			290			295										
113	ccc	tcc	tac	aac	ctg	acc	ttc	cac	tcc	cag	aac	gtc	ctg	ctc	atc	964	
114	Pro	Ser	Tyr	Asn	Leu	Thr	Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Ile		
115	300			305			310										
117	aca	ctg	ata	acc	aac	act	gag	cgg	cg	cat	ccc	ggc	ttt	gag	gcc	acc	1012
118	Thr	Leu	Ile	Thr	Asn	Thr	Glu	Arg	Arg	His	Pro	Gly	Phe	Glu	Ala	Thr	
119	315			320			325			330							
121	ttc	tcc	cag	ctg	cct	agg	atg	agc	agc	tgt	gga	ggc	cgc	tta	cgt	aaa	1060
122	Phe	Phe	Gln	Leu	Pro	Arg	Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys	
123					335				340			345					
125	gcc	cag	ggg	aca	ttc	aac	agc	ccc	tac	tac	cca	ggc	cac	tac	cca	ccc	1108
126	Ala	Gln	Gly	Thr	Phe	Asn	Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	Pro	Pro	

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Output Set: N:\CRF4\08112003\J612466.raw

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131	365	370	375	
133	aag gtg agc ttc aaa ttc ttc tac ctg ctg gag ccc ggc gtg cct gcg			1204
134	Lys Val Ser Phe Lys Phe Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala			
135	380	385	390	
137	ggc acc tgc ccc aag gac tac gtg gag atc aat ggg gag aaa tac tgc			1252
138	Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys			
139	395	400	405	410
141	gga gag agg tcc cag ttc gtc acc agc aac agc aac aag atc aca			1300
142	Gly Glu Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr			
143	415	420	425	
145	gtt cgc ttc cac tca gat cag tcc tac acc gac acc ggc ttc tta gct			1348
146	Val Arg Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala			
147	430	435	440	
149	gaa tac ctc tcc tac gac tcc agt gac cca tgc ccg ggg cag ttc acg			1396
150	Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr			
151	445	450	455	
153	tgc cgc acg ggg cgg tgt atc cgg aag gag ctg cgc tgt gat ggc tgg			1444
154	Cys Arg Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp			
155	460	465	470	
157	gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc			1492
158	Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala			
159	475	480	485	490
161	ggc cac cag ttc acg tgc aag aac aag ttc tgc aag ccc ctc ttc tgg			1540
162	Gly His Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp			
163	495	500	505	
165	gtc tgc gac agt gtg aac gac tgc gga gac aac agc gac gag cag ggg			1588
166	Val Cys Asp Ser Val Asn Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly			
167	510	515	520	
169	tgc agt tgt ccg gcc cag acc ttc agg tgt tcc aat ggg aag tgc ctc			1636
170	Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu			
171	525	530	535	
173	tcg aaa agc cag cag tgc aat ggg aag gac gac tgt ggg gac ggg tcc			1684
174	Ser Lys Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser			
175	540	545	550	
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179	555	560	565	570
181	acc tac cgc tgc ctc aat ggg ctc tgc ttg agc aag ggc aac cct gag			1780
182	Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu			
183	575	580	585	
185	tgt gac ggg aag gag gac tgt agc gac ggc tca gat gag aag gac tgc			1828
186	Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys			
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189	gac tgt ggg ctg cgg tca ttc acg aga cag gct cgt gtt gtt ggg ggc			1876
190	Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly			
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194 Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala	
195 620 625 630	1972
197 ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg	
198 Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp	
199 635 640 645 650	2020
201 ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac	
202 Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr	
203 655 660 665	2068
205 tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc	
206 Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser	
207 670 675 680	2116
209 cag cgc agc gcc cct ggg gtc cag gag cgc agg ctc aag cgc atc atc	
210 Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile	
211 685 690 695	2164
213 tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gct ctg	
214 Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu	
215 700 705 710	2212
217 ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtc cgg ccc atc	
218 Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile	
219 715 720 725 730	2260
221 tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg	
222 Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp	
223 735 740 745	2308
225 gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc	
226 Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile	
227 750 755 760	2356
229 ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac	
230 Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn	
231 765 770 775	2404
233 ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtc ggc ttc ctc	
234 Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu	
235 780 785 790	2452
237 agc ggc ggc gtc gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc	
238 Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser	
239 795 800 805 810	2500
241 agc gtg gag gcg gat ggg cgg atc ttc cag gcc ggt gtc gtc agc tgg	
242 Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly Val Val Ser Trp	
243 815 820 825	2548
245 gga gac ggc tgc gct cag agg aac aag cca ggc gtc tac aca agg ctc	
246 Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu	
247 830 835 840 845	2719
249 cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta gggggccgggg	2599
250 Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val	
251 845 850 855	2779
253 ccacccaaat gtgtacacct gcggggccac ccatacgcca ccccaagtgtg cacgcctgca	2659
254 ggctggagac tggaccgctg actgcaccag cggcccccaga acatacactg tgaactcaat	
255 ctccaggct ccaaactgc cttagaaaacc tctcgatccc tcagcctcca aagtggagct	2839
256 gggaggtaga aggggaggac actgggtgtt ctactgaccc aactgggggc aaaggtttga	

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259 ggctgccccgaa tctgggtgtt gggcccttg ggcacgctc ttgagaaagc ccaggctcg 3019
260 aggaccctgg aaaacagacg ggctgagac taaaattttt ttaccagctc ccagggtgga 3079
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273 20 25 30
274 Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
275 35 40 45
276 Lys His Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
277 50 55 60
278 Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
279 65 70 75 80
280 Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
281 85 90 95
282 Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
283 100 105 110
284 Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
285 115 120 125
286 Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
287 130 135 140
288 Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
289 145 150 155 160
290 Ile Pro Gln His Leu Val Glu Ala Glu Arg Val Met Ala Glu Glu
291 165 170 175
292 Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
293 180 185 190
294 Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
295 195 200 205
296 Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
297 210 215 220
298 Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
299 225 230 235 240
300 His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
301 245 250 255
302 Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
303 260 265 270
304 Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
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10/6/12, 466

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<211> LENGTH: 100

22123 TYPE: TRI
22133 ORGANISM:

<213> Homo Sapiens

2203 FEATURE

£2209 FEATURES.
£2233 OTHER IN

OTHER PROTEINS
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 35 40 45
 Ala Ser Cys Trp Val Leu Gly Trp Lys Glu Pro Gln Asp Arg Val Pro
 50 55 60
 Val Ala Ala Ala Val Ser Ile Leu Thr Gln Arg Ile Cys Asp Cys Leu
 65 70 75 80
 Tyr Gln Gly Ile Leu Pro Pro Gly Thr Leu Cys Val Leu Tyr Ala Glu
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What response is the valid one?

lude (2207-2237)
section
and explanation
of source
material on
(2237) line

<210> SEQ ID NO 22

<211> LENGTH: 37

<212> TYPE: PRT

<212> ~~ORGANISM~~: Artificial Sequence

~~213~~ **Homo Sapien**

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SEQUENCE: 22 Asn Asp Ser Arg Trp Ser Leu Leu Cys Gln Glu Glu Gly Thr Trp Phe
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 20 25 30
 Phe Phe Pro Leu Gln
 35